

REPLACEMENT SHEET

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FIGURE 1A

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1 atggcccaag cccctgcctg gctcctgctg tggatgagag cgggagtgct
51 gcttgcctcc ggcacccagc sgggcatccg gctgcctctg cgcagcggcc
101 tgggggggccc ccccttgggg ctggggctgc cccgggagac cgcagcagag
151 cccgaggagc cgggcgggag gggcagcttc gtggagatgg tggacaagct
201 gggggggcag tgggggcagg gctactacgt gggatganc gtggggcagc
251 cccggcagac gctcaacatc ctggtggata cgggcagcag taactttgca
301 gtgggtgctg ccccccaccc ctctctgcat cgtactaac agaggcagct
351 gtccagcaca tccggggacc tccgggaagg tgtgtatgtg cctacaccc
401 agggcaagtg ggaaggggag ctggggcacc acctggtaag catccccc
451 gggcccaacg tccctgtgct tgcacacatc gctgcctc ctaaatcaga
501 caagtctctc atcaacggct ccaactggga aggcattctg gggctggct
551 atgctgagat tggcaggatc attggaggta tgcaccctc gctgtacaca
601 ggcagctctc ggtatacacc catccggcgg ggtgggtatt atgaggtcat
651 catgtgtcgg ggggagatca atggacagga tctgaaaatg gactgcaagg
701 agtacaacta tgacagagag attgtggaca ggggcacac caaccttcgt
751 ttgcccaga aagtgtttga agctgcagtc aatccatca aggcagctc
801 ctccacggag aagttcctct atggtttctg gctaggagag cagctgggtg
851 gctggcaagc aggcacaccc ccttggaaaca ttttccagc catctcactc
901 taccataatg gtgaggttac caaccagtc tccgcacaca ccatcttcc
951 gcagcaatac ctgcccgcag tggaaagatg ggcacagtc caagcagact
1001 gttcaaatgt tgcacatcca cagtcatcca cgggcactgt tatgggagct
1051 gttatcatgg agggcttcca cgttgtcttt gctgggccc gaaacgaat
1101 tggctttgct gtcagcgttc gccatgttca ccatgagtc aggaacggag
1151 cgggtggagg cccctttgtc acctggaca tggaaagact tgggtacaa
1201 attccacaga cagatgagtc aacctcatg acctagcct atgtcatggc
1251 tgcacatctg gccctctcca tgcctgacct ctgctcatg gtgtgtcagt
1301 ggcgctgct cccgtgctg cgcagcagc atgatgact tgcgtatgac
1351 auctccctgc tgaagtga

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FIGURE 1B

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BACE501: 1 MAQALFWLLWNGAGVLPARTQMGIRLPLRSLGGOAPLGLRLFPETDEEPPEPQPGSP 60
MAQALFWLLWNGAGVLPARTQMGIRLPLRSLGGOAPLGLRLFPETDEEPPEPQPGSP
BACE455: 1 MAQALFWLLWNGAGVLPARTQMGIRLPLRSLGGOAPLGLRLFPETDEEPPEPQPGSP 60
BACE501: 61 VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVDTGSENFVGAAPHFPLHRYVQQLSST 120
VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVDTGSENFVGAAPHFPLHRYVQQLSST
BACE455: 61 VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVDTGSENFVGAAPHFPLHRYVQQLSST 120
BACE501: 121 YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL 180
YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL
BACE455: 121 YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL 180
BACE501: 181 GLAYAEIARPDOSLEPFPU3LVKQTHVPLNLSLQCGAGFPLNQSEVLASVQSMIGGI 240
GLAYAEIARPDOSLEPFPU3LVKQTHVPLNLSLQCGAGFPLNQSEVLASVQSMIGGI
BACE455: 181 GLAYAEIARPDOSLEPFPU3LVKQTHVPLNLSLQCGAGFPLNQSEVLASVQSMIGGI 240
BACE501: 241 DHSLYTGLWYTPINREWYVEVIIVRVBINGQDLMDCKEYNYDKSIVDSGTTNLRPKK 300
DHSLYTGLWYTPINREWYVEVIIVRVBINGQDLMDCKEYNYDKSIVDSGTTNLRPKK
BACE455: 241 DHSLYTGLWYTPINREWYVEVIIVRVBINGQDLMDCKEYNYDKSIVDSGTTNLRPKK 300
BACE501: 301 VFPAAYKSIKASSTKFPDGPWLGEQLVCWQAGTTFWNIFFVISLXLMGEVTVNQSPRIT 360
VFPAAYKSIKASSTKFPDGPWLGEQLVCWQAGTTFWNIFFVISLXLMGEVTVNQSPRIT
BACE455: 301 VFPAAYKSIKASSTKFPDGPWLGEQLVCWQAGTTFWNIFFVISLXLMGEVTVNQSPRIT 360
BACE501: 361 ILPQQYLRFVBDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVPDRAKFAIGPAVSAC 420
ILPQQYLRFVBDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVPDRAKFAIGPAVSAC
BACE455: 361 ILPQQYLRFVBDVATSDQDCYKFAISQSSTGTVMGAVIMEGFYVVPDRAKFAIGPAVSAC 420
BACE501: 421 HVHDEFRTAAVEGFPVTLDMEDCGYNIPTQDESTLMTIAYVMAALCALPMLPLCLMVCQW 480
HVHDEFRTAAVEGFPVTLDMEDCGYNIPTQDESTLMTIAYVMAALCALPMLPLCLMVCQW
BACE455: 421 HVHDEFRTAAVEGFPVTLDMEDCGYNIPTQDESTLMTIAYVMAALCALPMLPLCLMVCQW 480
BACE501: 481 RCLRCLRQGHODFAODISLLK 501
RCLRCLRQGHODFAODISLLK
BACE455: 481 RCLRCLRQGHODFAODISLLK 501

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REPLACEMENT SHEET

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FIGURE 2A

FIGURE 2B

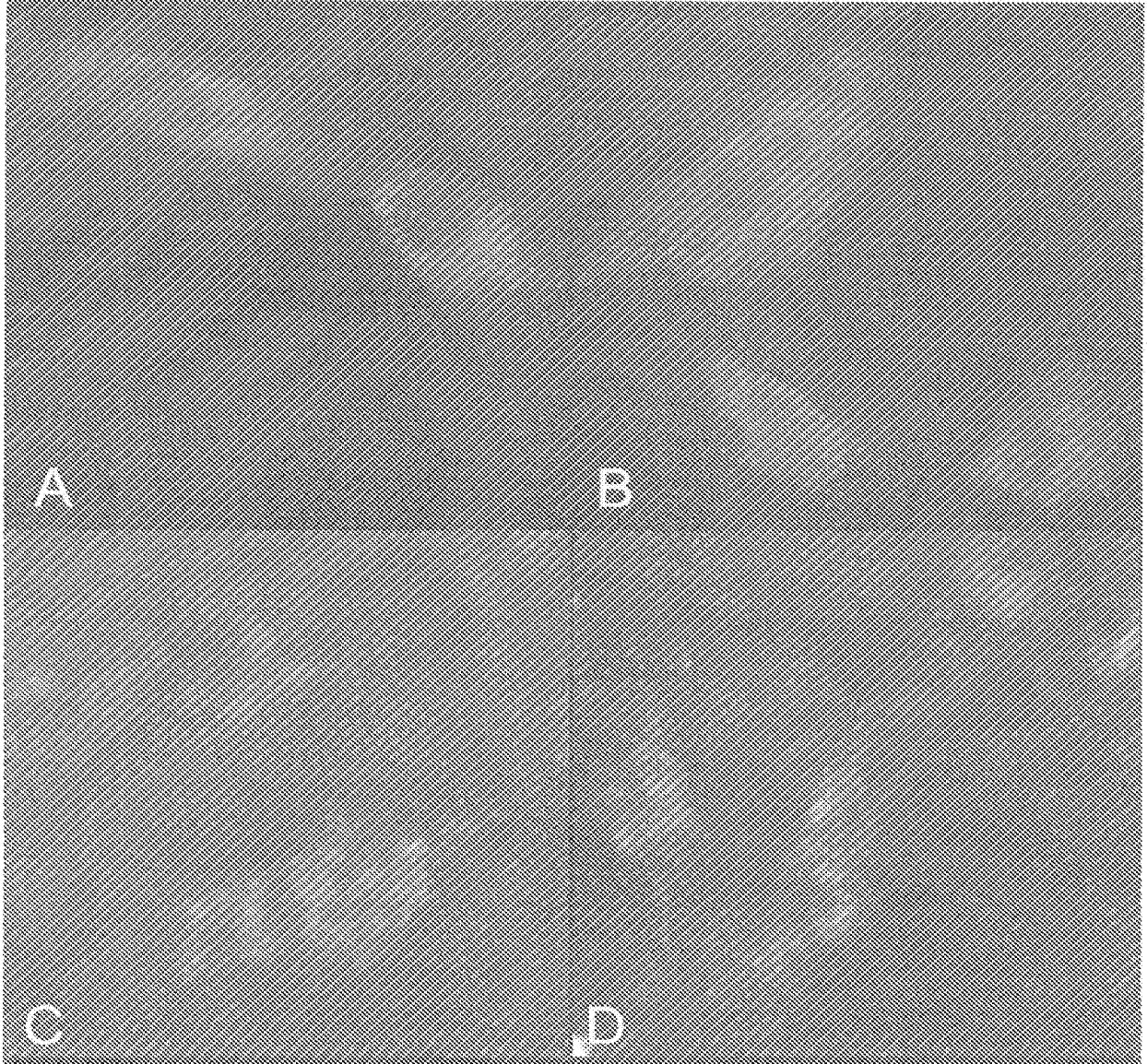


FIGURE 2C

FIGURE 2D

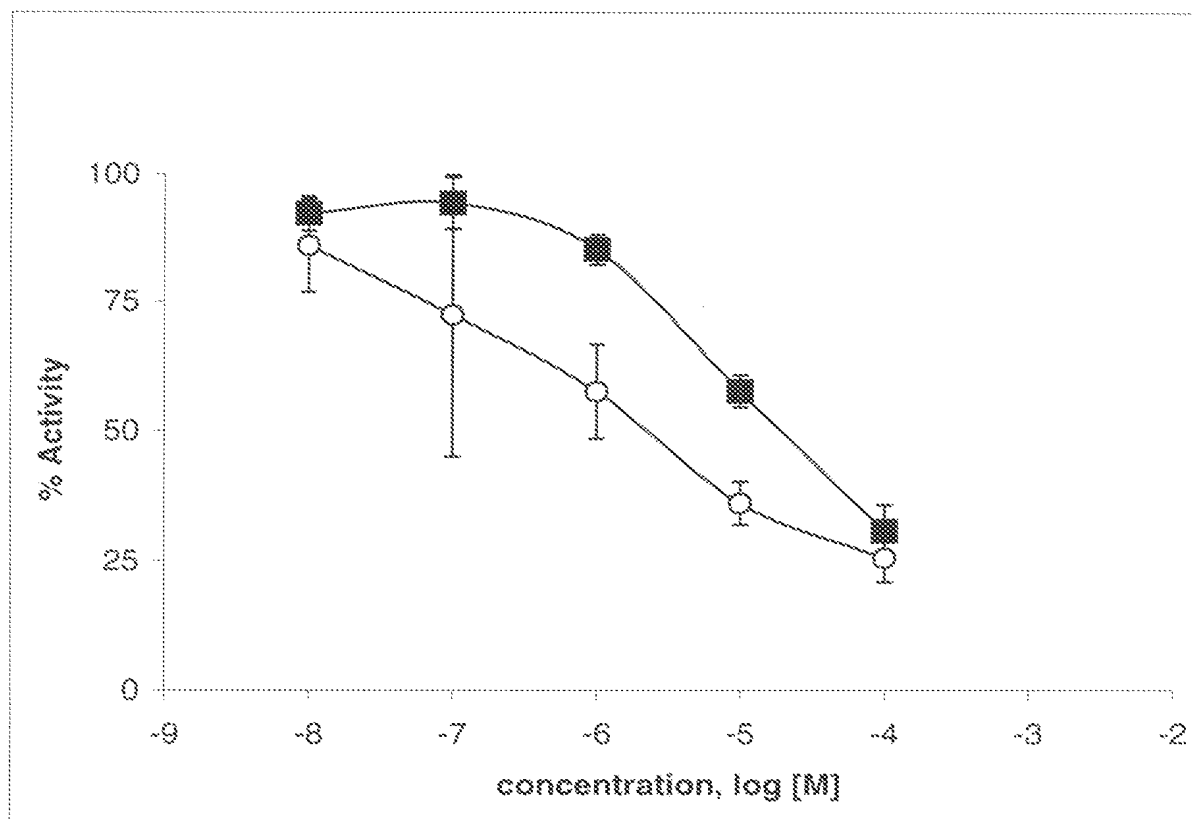


Figure 3

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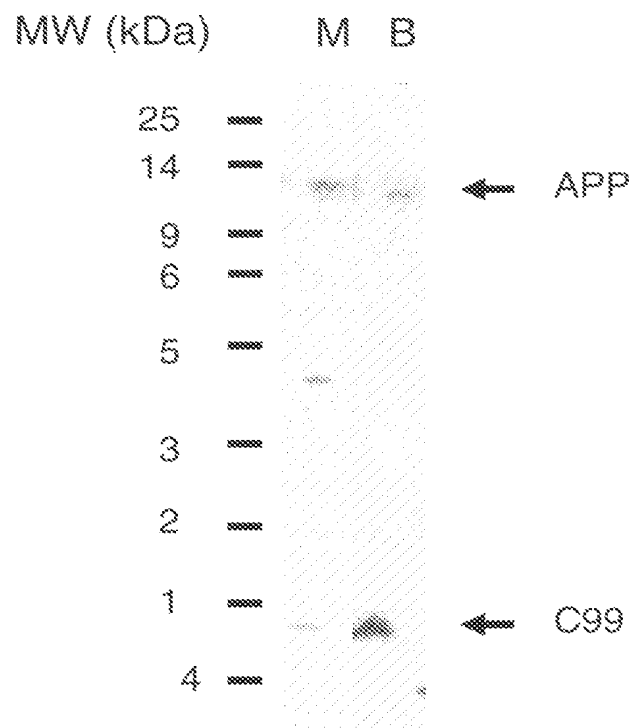


Figure 4

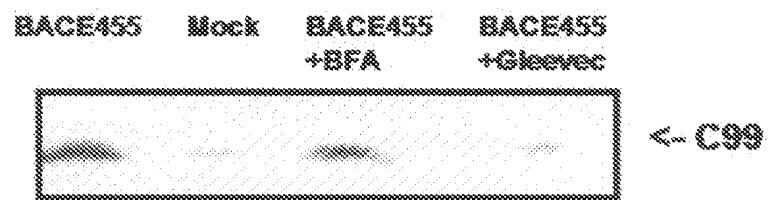


Figure 5